

SEQUENCE LISTING

<110> Caniggia, Isabella
Post, Martin
Lye, Stephen

<120> METHODS TO DIAGNOSE A REQUIRED REGULATION OF TROPHOBLAST

<130> 11757.38USWO

<140> US 09/380,662
<141> 1999-12-21

<150> PCT/CA98/00180
<151> 1998-03-05

<150> US 60/039,919
<151> 1997-03-07

<160> 24

<170> PatentIn version 3.0

<210> 1
<211> 16
<212> DNA
<213> Homo sapiens

<400> 1
cctttgcaag tgcatc 16

<210> 2
<211> 16
<212> DNA
<213> Homo sapiens

<400> 2
gatgcacttg caaagg 16

<210> 3
<211> 16
<212> DNA
<213> Homo sapiens

<400> 3
gcgtgcccgcg gtccat 16

<210> 4
<211> 16
<212> DNA
<213> Homo sapiens

<400> 4
atggaccgcg gcacgc 16

<210> 5

<211> 16
<212> DNA
<213> Homo sapiens

<400> 5
gcggggctcg ttccag

16

<210> 6
<211> 22
<212> DNA
<213> Homo sapiens

<400> 6
gccctggaca ccaactattg ct

22

<210> 7
<211> 22
<212> DNA
<213> Homo sapiens

<400> 7
aggctccaaa ttaggggca gg

22

<210> 8
<211> 20
<212> DNA
<213> Homo sapiens

<400> 8
catctggtcc cggcggcgct

20

<210> 9
<211> 18
<212> DNA
<213> Homo sapiens

<400> 9
gacgattctg aagttaggg

18

<210> 10
<211> 21
<212> DNA
<213> Homo sapiens

<400> 10
caaagggttc tggtggtcat g

21

<210> 11
<211> 22
<212> DNA
<213> Homo sapiens

<400> 11
cttagaggtt atcccccttgg gg

22

<210> 12
<211> 20
<212> DNA
<213> Homo sapiens

<400> 12
cttctacaaat gagctgggtg

20

<210> 13
<211> 20
<212> DNA
<213> Homo sapiens

<400> 13
tcatgaggta gtcagtcagg

20

<210> 14
<211> 16
<212> DNA
<213> Homo sapiens

<400> 14
ccccgagggc ggcatg

16

<210> 15
<211> 16
<212> DNA
<213> Homo sapiens

<400> 15
catgcggccc tcgggg

16

<210> 16
<211> 16
<212> DNA
<213> Homo sapiens

<400> 16
cacacagtac tgcattg

16

<210> 17
<211> 16
<212> DNA
<213> Homo sapiens

<400> 17
catgcactac tgtgtg

16

<210> 18
<211> 16
<212> DNA
<213> Homo sapiens

<400> 18 cctttgcaga tgcatc	16
<210> 19 <211> 16 <212> DNA <213> Homo sapiens	
<400> 19 gatgcacttg caaagg	16
<210> 20 <211> 2574 <212> DNA <213> Homo sapiens	
<220> <221> CDS <222> (254)...(1492)	
<400> 20 cctgtttaga cacatggaca acaatccccag cgctacaagg cacacagtcc gcttcctcg cctcagggtt gccagcgctt cctggaaagtc ctgaagctct cgcagtgcag tgagttcatg caccttcttg ccaaggcctca gtctttggga tctggggagg ccgcctggtt ttccctccctc cttctgcacg tctgctgggg tctcttcctc tccaggccctt gccgtcccccc tgccctctct tcccagctca cac atg aag atg cac ttg caa agg gct ctg gtg gtc ctg Met Lys Met His Leu Gln Arg Ala Leu Val Val Leu 1 5 10	60 120 180 240 289
gcc ctg ctg aac ttt gcc acg gtc agc ctc tct ctg tcc act tgc acc Ala Leu Leu Asn Phe Ala Thr Val Ser Leu Ser Leu Thr Cys Thr 15 20 25	337
acc ttg gac ttc ggc cac atc aag aag aag agg gtg gaa gcc att agg Thr Leu Asp Phe Gly His Ile Lys Lys Arg Val Glu Ala Ile Arg 30 35 40	385
gga cag atc ttg agc aag ctc agg ctc acc agc ccc cct gag cca acg Gly Gln Ile Leu Ser Lys Leu Arg Leu Thr Ser Pro Pro Glu Pro Thr 45 50 55 60	433
gtg atg acc cac gtc ccc tat cag gtc ctg gcc ctt tac sac agc acc Val Met Thr His Val Pro Tyr Gln Val Ala Leu Tyr Asn Ser Thr 65 70 75	481
cgg gag ctg ctg gag gag atg cat ggg gag agg gag gaa ggc tgc acc Arg Glu Leu Leu Glu Glu Met His Gly Glu Arg Glu Glu Gly Cys Thr 80 85 90	529
cag gaa aac acc gag tcg gaa tac tat gcc aaa gaa atc cat aaa ttc Gln Glu Asn Thr Glu Ser Glu Tyr Tyr Ala Lys Glu Ile His Lys Phe 95 100 105	577

gac atg atc cag ggg ctg gcg gag cac aac gaa ctg gct gtc tgc cct Asp Met Ile Gln Gly Leu Ala Glu His Asn Glu Leu Ala Val Cys Pro 110 115 120	625
aaa gga att acc tcc aag gtt ttc cgc ttc aat gtg tcc tca gtg gag Lys Gly Ile Thr Ser Lys Val Phe Arg Phe Asn Val Ser Ser Val Glu 125 130 135 140	673
aaa aat aga acc aac cta ttc cga gca gaa ttc cgg gtc ttg cgg gtg Lys Asn Arg Thr Asn Leu Phe Arg Ala Glu Phe Arg Val Leu Arg Val 145 150 155	721
ccc aac ccc agc tct aag cgg aat gag cag agg atc gag ctc ttc cag Pro Asn Pro Ser Ser Lys Arg Asn Glu Gln Arg Ile Glu Leu Phe Gln 160 165 170	769
atc ctt cgg cca gat gag cac att gcc aaa cag cgc tat atc ggt ggc Ile Leu Arg Pro Asp Glu His Ile Ala Lys Gln Arg Tyr Ile Gly Gly 175 180 185	817
aag aat ctg ccc aca cgg ggc act gcc gag tgg ctg tcc ttt gat gtc Lys Asn Leu Pro Thr Arg Gly Thr Ala Glu Trp Leu Ser Phe Asp Val 190 195 200	865
act gac act gtg cgt gag tgg ctg ttg aga aga gag tcc aac tta ggt Thr Asp Thr Val Arg Glu Trp Leu Leu Arg Arg Glu Ser Asn Leu Gly 205 210 215 220	913
cta gaa atc agc att cac tgt cca tgt cac acc ttt cag ccc aat gga Leu Glu Ile Ser Ile His Cys Pro Cys His Thr Phe Gln Pro Asn Gly 225 230 235	961
gat atc ctg gaa aac att cac gag gtg atg gaa atc aaa ttc aaa ggc Asp Ile Leu Glu Asn Ile His Glu Val Met Glu Ile Lys Phe Lys Gly 240 245 250	1009
gtg gac aat gag gat gac cat ggc cgt gga gat ctg ggg cgc ctc aag Val Asn Asn Glu Asp Asp His Gly Arg Gly Asp Leu Gly Arg Leu Lys 255 260 265	1057
aag cag aag gat cac cac aac cct cat cta atc ctc atg atg att ccc Lys Gln Lys Asp His His Asn Pro His Leu Ile Leu Met Met Ile Pro 270 275 280	1105
cca cac cgg ctc gac aac ccg ggc cag ggg ggt cag agg aag aag cgg Pro His Arg Leu Asp Asn Pro Gly Gln Gly Gln Arg Lys Lys Arg 285 290 295 300	1153
gct ttg gac acc aat tac tgc ttc cgc aac ttg gag gag aac tgc tgt Ala Leu Asp Thr Asn Tyr Cys Phe Arg Asn Leu Glu Asn Cys Cys 305 310 315	1201
gtg cgc ccc ctc tac att gac ttc cga cag gat ctg ggc tgg aag tgg Val Arg Pro Leu Tyr Ile Asp Phe Arg Gln Asp Leu Gly Trp Lys Trp 320 325 330	1249
gtc cat gaa cct aag ggc tac tat gcc aac ttc tgc tca ggc cct tgc Val His Glu Pro Lys Gly Tyr Ala Asn Phe Cys Ser Gly Pro Cys 335 340 345	1297

cca tac ctc cgc agt gca gac aca acc cac agc acg gtg ctg gga ctg Pro Tyr Leu Arg Ser Ala Asp Thr Thr His Ser Thr Val Leu Gly Leu 350 355 360	1345
tac aac act ctg aac cct gaa gca tct gcc tcg cct tgc tgc gtg ccc Tyr Asn Thr Leu Asn Pro Glu Ala Ser Ala Ser Pro Cys Cys Val Pro 365 370 375 380	1393
cag gac ctg gag ccc ctg acc atc ctg tac tat gtt ggg agg acc ccc Gln Asp Leu Glu Pro Leu Thr Ile Leu Tyr Tyr Val Gly Arg Thr Pro 385 390 395	1441
aaa gtg gag cag ctc tcc aac atg gtg gtg aag tct tgt aaa tgt agc Lys Val Glu Gln Leu Ser Asn Met Val Val Lys Ser Cys Lys Cys Ser 400 405 410	1489
tga gaccccacgt gcgcacagaga gaggggagag agaaccacca ctgcctgact gccccgtcct cggaaacac acaagcaaca aacctcaactg agaggcctgg agccccacaac ctteggctcc gggcaaatgg ctgagatgga ggtttccctt tggAACATTt ctttcttgct ggctctgaga atcacggtgg taaagaaagt gtgggttgg tttaggaaag gctgaactct tcagaacaca cagactttct gtgacgcaga cagagggat gggatagag gaaagggatg gtaagtgag attttgtgtg gcaatggat ttggctacc ctAAAGGGAG aaggaagggc agagaatggc tgggtcaggg ccagactgga agacacttca gatctgaggt tggatttgct cattgtgtt ccacatctgc tctaggaaat ctggattatg ttatacaagg caagcattt ttttttaaa gacaggttac gaagacaaag tcccagaatt gtatctcata ctgtctggga ttaaggcAA atctattact tttgcaaaact gtcctctaca tcaattaaca tcgtgggtca ctacagggag AAAATCCAGG tcatgcagtt cctggcccat caactgtatt gggccttttg gatatgtgtt acgcagaaga aagggtggaa atcaaccctc tccgtctgc cctctgggtc cctccctctca cctctccctc gatcatatTTT ccccttggac acgtggtag acgccttcca ggtcaggatg cacatTTCTG gattgtggtt ccatgcagcc ttggggcatt atgggtcttc ccccacttcc cctccaagac cctgtgttca tttgggtgttcc ctggaaacgag gtgttacaac atgtgaggca ttccggggaaag ctgcacatgt gcccacacagt gacttggccc cagacgcata gactgaggta taaagacaag tatgaatatt actctaaaaa tctttgtata aataaaatatt tttggggcat cctggatgtat ttcatTTCTG ggaatattgt ttctagaaca gtaaaagcct tattctaagg tg	1542 1602 1662 1722 1782 1842 1902 1962 2022 2082 2142 2202 2262 2322 2382 2442 2502 2562 2574

<210> 21
<211> 412
<212> PRT
<213> Homo sapiens

<400> 21

Met Lys Met His Leu Gln Arg Ala Leu Val Val Leu Ala Leu Leu Asn
1 5 10 15

Phe Ala Thr Val Ser Leu Ser Leu Ser Thr Cys Thr Thr Leu Asp Phe
20 25 30

Gly His Ile Lys Lys Lys Arg Val Glu Ala Ile Arg Gly Gln Ile Leu
35 40 45

Ser Lys Leu Arg Leu Thr Ser Pro Pro Glu Pro Thr Val Met Thr His
50 55 60

Val Pro Tyr Gln Val Leu Ala Leu Tyr Asn Ser Thr Arg Glu Leu Leu
65 70 75 80

Glu Glu Met His Gly Glu Arg Glu Glu Gly Cys Thr Gln Glu Asn Thr
85 90 95

Glu Ser Glu Tyr Tyr Ala Lys Glu Ile His Lys Phe Asp Met Ile Gln
100 105 110

Gly Leu Ala Glu His Asn Glu Leu Ala Val Cys Pro Lys Gly Ile Thr
115 120 125

Ser Lys Val Phe Arg Phe Asn Val Ser Ser Val Glu Lys Asn Arg Thr
130 135 140

Asn Leu Phe Arg Ala Glu Phe Arg Val Leu Arg Val Pro Asn Pro Ser
145 150 155 160

Ser Lys Arg Asn Glu Gln Arg Ile Glu Leu Phe Gln Ile Leu Arg Pro
165 170 175

Asp Glu His Ile Ala Lys Gln Arg Tyr Ile Gly Gly Lys Asn Leu Pro
180 185 190

Thr Arg Gly Thr Ala Glu Trp Leu Ser Phe Asp Val Thr Asp Thr Val
195 200 205

Arg Glu Trp Leu Leu Arg Arg Glu Ser Asn Leu Gly Leu Glu Ile Ser
210 215 220

Ile His Cys Pro Cys His Thr Phe Gln Pro Asn Gly Asp Ile Leu Glu
225 230 235 240

Asn Ile His Glu Val Met Glu Ile Lys Phe Lys Gly Val Asp Asn Glu
245 250 255

Asp Asp His Gly Arg Gly Asp Leu Gly Arg Leu Lys Lys Gln Lys Asp
260 265 270

His His Asn Pro His Leu Ile Leu Met Met Ile Pro Pro His Arg Leu
275 280 285

Asp Asn Pro Gly Gln Gly Gln Arg Lys Lys Arg Ala Leu Asp Thr
290 295 300

Asn Tyr Cys Phe Arg Asn Leu Glu Glu Asn Cys Cys Val Arg Pro Leu
305 310 315 320

Tyr Ile Asp Phe Arg Gln Asp Leu Gly Trp Lys Trp Val His Glu Pro
325 330 335

Lys Gly Tyr Tyr Ala Asn Phe Cys Ser Gly Pro Cys Pro Tyr Leu Arg
340 345 350

Ser Ala Asp Thr Thr His Ser Thr Val Leu Gly Leu Tyr Asn Thr Leu
355 360 365

Asn Pro Glu Ala Ser Ala Ser Pro Cys Cys Val Pro Gln Asp Leu Glu
370 375 380

Pro Leu Thr Ile Leu Tyr Tyr Val Gly Arg Thr Pro Lys Val Glu Gln
385 390 395 400

Leu Ser Asn Met Val Val Lys Ser Cys Lys Cys Ser
405 410

<210> 22
<211> 3678
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (29)...(2509)

<400> 22
gtgaagacat cgcccccc gattcacc atg gag ggc gcc ggc ggc gcg aac
Met Glu Gly Ala Gly Gly Ala Asn
1 5

52

gac aag aaa aag ata agt tct gaa cgt cga aaa gaa aag tct cga gat Asp Lys Lys Lys Ile Ser Ser Glu Arg Arg Lys Glu Lys Ser Arg Asp 10 15 20	100
gca gcc aga tct cgg cga agt aaa gaa tct gaa gtt ttt tat gag ctt Ala Ala Arg Ser Arg Ser Lys Glu Ser Glu Val Phe Tyr Glu Leu 25 30 35 40	148
gct cat cag ttg cca ctt cca cat aat gtg agt tcg cat ctt gat aag Ala His Gln Leu Pro Leu Pro His Asn Val Ser Ser His Leu Asp Lys 45 50 55	196
gcc tct gtg atg agg ctt acc atc agc tat ttg cgt gtg agg aaa ctt Ala Ser Val Met Arg Leu Thr Ile Ser Tyr Leu Arg Val Arg Lys Leu 60 65 70	244
ctg gat gct ggt gat ttg gat att gaa gat gac atg aaa gca cag atg Leu Asp Ala Gly Asp Leu Asp Ile Glu Asp Asp Met Lys Ala Gln Met 75 80 85	292
aat tgc ttt tat ttg aaa gcc ttg gat ggt ttt gtt atg gtt ctc aca Asn Cys Phe Tyr Leu Lys Ala Leu Asp Gly Phe Val Met Val Leu Thr 90 95 100	340
gat gat ggt gac atg att tac att tct gat aat gtg aac aaa tac atg Asp Asp Gly Asp Met Ile Tyr Ile Ser Asp Asn Val Asn Lys Tyr Met 105 110 115 120	388
gga tta act cag ttt gaa cta act gga cac agt gtg ttt gat ttt act Gly Leu Thr Gln Phe Glu Leu Thr Gly His Ser Val Phe Asp Phe Thr 125 130 135	436
cat cca tgt gac cat gag gaa atg aga gaa atg ctt aca cac aga aat His Pro Cys Asp His Glu Glu Met Arg Glu Met Leu Thr His Arg Asn 140 145 150	484
ggc ctt gtg aaa aag ggt aaa gaa caa aac aca cag cga agc ttt ttt Gly Leu Val Lys Lys Gly Lys Glu Gln Asn Thr Gln Arg Ser Phe Phe 155 160 165	532
ctc aga atg aag tgt acc cta act agc cga gga aga act atg aac ata Leu Arg Met Lys Cys Thr Leu Thr Ser Arg Gly Arg Thr Met Asn Ile 170 175 180	580
aag tct gca aca tgg aag gta ttg cac tgc aca ggc cac att cac gta Lys Ser Ala Thr Trp Lys Val Leu His Cys Thr Gly His Ile His Val 185 190 195 200	628
tat gat acc aac agt aac caa cct cag tgt ggg tat aag aaa cca cct Tyr Asp Thr Asn Ser Asn Gln Pro Gln Cys Gly Tyr Lys Lys Pro Pro 205 210 215	676
atg acc tgc ttg gtg ctg att tgt gaa ccc att cct cac cca tca aat Met Thr Cys Leu Val Leu Ile Cys Glu Pro Ile Pro His Pro Ser Asn 220 225 230	724
att gaa att cct tta gat agc aag act ttc ctc agt cga cac agc ctg Ile Glu Ile Pro Leu Asp Ser Lys Thr Phe Leu Ser Arg His Ser Leu 235 240 245	772

gat atg aaa ttt tct tat tgt gat gaa aga att acc gaa ttg atg gga Asp Met Lys Phe Ser Tyr Cys Asp Glu Arg Ile Thr Glu Leu Met Gly 250 255 260	820
tat gag cca gaa gaa ctt tta ggc cgc tca att tat gaa tat tat cat Tyr Glu Pro Glu Glu Leu Leu Gly Arg Ser Ile Tyr Glu Tyr Tyr His 265 270 275 280	868
gct ttg gac tct gat cat ctg acc aaa act cat cat gat atg ttt act Ala Leu Asp Ser Asp His Leu Thr Lys Thr His His Asp Met Phe Thr 285 290 295	916
aaa gga caa gtc acc aca gga cag tac agg atg ctt gcc aaa aga ggt Lys Gly Gln Val Thr Thr Gly Gln Tyr Arg Met Leu Ala Lys Arg Gly 300 305 310	964
gga tat gtc tgg gtt gaa act caa gca act gtc ata tat aac acc aag Gly Tyr Val Trp Val Glu Thr Gln Ala Thr Val Ile Tyr Asn Thr Lys 315 320 325	1012
aat tct caa cca cag tgc att gta tgt gtg aat tac gtt gtg agt ggt Asn Ser Gln Pro Gln Cys Ile Val Cys Val Asn Tyr Val Val Ser Gly 330 335 340	1060
att att cag cac gac ttg att ttc tcc ctt caa caa aca gaa tgt gtc Ile Ile Gln His Asp Leu Ile Phe Ser Leu Gln Gln Thr Glu Cys Val 345 350 355 360	1108
ctt aaa ccg gtt gaa tct tca gat atg aaa atg act cag cta ttc acc Leu Lys Pro Val Glu Ser Ser Asp Met Lys Met Thr Gln Leu Phe Thr 365 370 375	1156
aaa gtt gaa tca gaa gat aca agt agc ctc ttt gac aaa ctt aag aag Lys Val Glu Ser Glu Asp Thr Ser Ser Leu Phe Asp Lys Leu Lys Lys 380 385 390	1204
gaa cct gat gct tta act ttg ctg gcc cca gcc gct gga gac aca atc Glu Pro Asp Ala Leu Thr Leu Leu Ala Pro Ala Ala Gly Asp Thr Ile 395 400 405	1252
ata tct tta gat ttt ggc agc aac gac aca gaa act gat gac cag caa Ile Ser Leu Asp Phe Gly Ser Asn Asp Thr Glu Thr Asp Asp Gln Gln 410 415 420	1300
ctt gag gaa gta cca tta tat aat gat gta atg ctc ccc tca ccc aac Leu Glu Glu Val Pro Leu Tyr Asn Asp Val Met Leu Pro Ser Pro Asn 425 430 435 440	1348
gaa aaa tta cag aat ata aat ttg gca atg tct cca tta ccc acc gct Glu Lys Leu Gln Asn Ile Asn Leu Ala Met Ser Pro Leu Pro Thr Ala 445 450 455	1396
gaa acg cca aag cca ctt cga agt agt gct gac cct gca ctc aat caa Glu Thr Pro Lys Pro Leu Arg Ser Ser Ala Asp Pro Ala Leu Asn Gln 460 465 470	1444
gaa gtt gca tta aaa tta gaa cca aat cca gag tca ctg gaa ctt tct Glu Val Ala Leu Lys Leu Glu Pro Asn Pro Glu Ser Leu Glu Leu Ser 475 480 485	1492

ttt acc atg ccc cag att cag gat cag aca cct agt cct tcc gat gga Phe Thr Met Pro Gln Ile Gln Asp Gln Thr Pro Ser Pro Ser Asp Gly 490 495 500	1540
agc act aga caa agt tca cct gag cct aat agt ccc agt gaa tat tgt Ser Thr Arg Gln Ser Ser Pro Glu Pro Asn Ser Pro Ser Glu Tyr Cys 505 510 515 520	1588
ttt tat gtg gat agt gat atg gtc aat gaa ttc aag ttg gaa ttg gta Phe Tyr Val Asp Ser Asp Met Val Asn Glu Phe Lys Leu Glu Leu Val 525 530 535	1636
gaa aaa ctt ttt gct gaa gac aca gaa gca aag aac cca ttt tct act Glu Lys Leu Phe Ala Glu Asp Thr Glu Ala Lys Asn Pro Phe Ser Thr 540 545 550	1684
cag gac aca gat tta gac ttg gag atg tta gct ccc tat atc cca atg Gln Asp Thr Asp Leu Asp Leu Glu Met Leu Ala Pro Tyr Ile Pro Met 555 560 565	1732
gat gat gac ttc cag tta cgt tcc ttc gat cag ttg tca cca tta gaa Asp Asp Asp Phe Gln Leu Arg Ser Phe Asp Gln Leu Ser Pro Leu Glu 570 575 580	1780
agc agt tcc gca agc cct gaa agc gca agt cct caa agc aca gtt aca Ser Ser Ser Ala Ser Pro Glu Ser Ala Ser Pro Gln Ser Thr Val Thr 585 590 595 600	1828
gta ttc cag cag act caa ata caa gaa cct act gct aat gcc acc act Val Phe Gln Gln Thr Gln Ile Gln Glu Pro Thr Ala Asn Ala Thr Thr 605 610 615	1876
acc act gcc acc act gat gaa tta aaa aca gtg aca aaa gac cgt atg Thr Thr Ala Thr Asp Glu Leu Lys Thr Val Thr Lys Asp Arg Met 620 625 630	1924
gaa gac att aaa ata ttg att gca tct cca tct cct acc cac ata cat Glu Asp Ile Lys Ile Leu Ile Ala Ser Pro Ser Pro Thr His Ile His 635 640 645	1972
aaa gaa act act agt gcc aca tca tca cca tat aga gat act caa agt Lys Glu Thr Thr Ser Ala Thr Ser Ser Pro Tyr Arg Asp Thr Gln Ser 650 655 660	2020
cgg aca gcc tca cca aac aga gca gga aaa gga gtc ata gaa cag aca Arg Thr Ala Ser Pro Asn Arg Ala Gly Lys Gly Val Ile Glu Gln Thr 665 670 675 680	2068
gaa aaa tct cat cca aga agc cct aac gtg tta tct gtc gct ttg agt Glu Lys Ser His Pro Arg Ser Pro Asn Val Leu Ser Val Ala Leu Ser 685 690 695	2116
caa aga act aca gtt cct gag gaa gaa cta aat cca aag ata cta gct Gln Arg Thr Thr Val Pro Glu Glu Leu Asn Pro Lys Ile Leu Ala 700 705 710	2164
ttg cag aat gct cag aga aag cga aaa atg gaa cat gat ggt tca ctt Leu Gln Asn Ala Gln Arg Lys Arg Lys Met Glu His Asp Gly Ser Leu 715 720 725	2212

aataattgag taattttaga agcattattt taggaatata tagttgtcac agtaaatatc 3569
ttgttttc tatgtacatt gtacaaatcc ttcatccctt tggcttttg tggttggatc 3629
taacactaac tgtattgttt tgttacatca aataaacatc ttctgtgga 3678

<210> 23
<211> 826
<212> PRT
<213> Homo sapiens

<400> 23

Met Glu Gly Ala Gly Gly Ala Asn Asp Lys Lys Lys Ile Ser Ser Glu
1 5 10 15

Arg Arg Lys Glu Lys Ser Arg Asp Ala Ala Arg Ser Arg Arg Ser Lys
20 25 30

Glu Ser Glu Val Phe Tyr Glu Leu Ala His Gln Leu Pro Leu Pro His
35 40 45

Asn Val Ser Ser His Leu Asp Lys Ala Ser Val Met Arg Leu Thr Ile
50 55 60

Ser Tyr Leu Arg Val Arg Lys Leu Leu Asp Ala Gly Asp Leu Asp Ile
65 70 75 80

Glu Asp Asp Met Lys Ala Gln Met Asn Cys Phe Tyr Leu Lys Ala Leu
85 90 95

Asp Gly Phe Val Met Val Leu Thr Asp Asp Gly Asp Met Ile Tyr Ile
100 105 110

Ser Asp Asn Val Asn Lys Tyr Met Gly Leu Thr Gln Phe Glu Leu Thr
115 120 125

Gly His Ser Val Phe Asp Phe Thr His Pro Cys Asp His Glu Glu Met
130 135 140

Arg Glu Met Leu Thr His Arg Asn Gly Leu Val Lys Lys Gly Lys Glu
145 150 155 160

Gln Asn Thr Gln Arg Ser Phe Phe Leu Arg Met Lys Cys Thr Leu Thr
165 170 175

Ser Arg Gly Arg Thr Met Asn Ile Lys Ser Ala Thr Trp Lys Val Leu
180 185 190

His Cys Thr Gly His Ile His Val Tyr Asp Thr Asn Ser Asn Gln Pro
195 200 205

Gln Cys Gly Tyr Lys Lys Pro Pro Met Thr Cys Leu Val Leu Ile Cys
210 215 220

Glu Pro Ile Pro His Pro Ser Asn Ile Glu Ile Pro Leu Asp Ser Lys
225 230 235 240

Thr Phe Leu Ser Arg His Ser Leu Asp Met Lys Phe Ser Tyr Cys Asp
245 250 255

Glu Arg Ile Thr Glu Leu Met Gly Tyr Glu Pro Glu Glu Leu Leu Gly
260 265 270

Arg Ser Ile Tyr Glu Tyr Tyr His Ala Leu Asp Ser Asp His Leu Thr
275 280 285

Lys Thr His His Asp Met Phe Thr Lys Gly Gln Val Thr Thr Gly Gln
290 295 300

Tyr Arg Met Leu Ala Lys Arg Gly Gly Tyr Val Trp Val Glu Thr Gln
305 310 315 320

Ala Thr Val Ile Tyr Asn Thr Lys Asn Ser Gln Pro Gln Cys Ile Val
325 330 335

Cys Val Asn Tyr Val Val Ser Gly Ile Ile Gln His Asp Leu Ile Phe
340 345 350

Ser Leu Gln Gln Thr Glu Cys Val Leu Lys Pro Val Glu Ser Ser Asp
355 360 365

Met Lys Met Thr Gln Leu Phe Thr Lys Val Glu Ser Glu Asp Thr Ser
370 375 380

Ser Leu Phe Asp Lys Leu Lys Lys Glu Pro Asp Ala Leu Thr Leu Leu
385 390 395 400

Ala Pro Ala Ala Gly Asp Thr Ile Ile Ser Leu Asp Phe Gly Ser Asn
405 410 415

Asp Thr Glu Thr Asp Asp Gln Gln Leu Glu Glu Val Pro Leu Tyr Asn
420 425 430

Asp Val Met Leu Pro Ser Pro Asn Glu Lys Leu Gln Asn Ile Asn Leu
435 440 445

Ala Met Ser Pro Leu Pro Thr Ala Glu Thr Pro Lys Pro Leu Arg Ser
450 455 460

Ser Ala Asp Pro Ala Leu Asn Gln Glu Val Ala Leu Lys Leu Glu Pro
465 470 475 480

Asn Pro Glu Ser Leu Glu Leu Ser Phe Thr Met Pro Gln Ile Gln Asp
485 490 495

Gln Thr Pro Ser Pro Ser Asp Gly Ser Thr Arg Gln Ser Ser Pro Glu
500 505 510

Pro Asn Ser Pro Ser Glu Tyr Cys Phe Tyr Val Asp Ser Asp Met Val
515 520 525

Asn Glu Phe Lys Leu Glu Leu Val Glu Lys Leu Phe Ala Glu Asp Thr
530 535 540

Glu Ala Lys Asn Pro Phe Ser Thr Gln Asp Thr Asp Leu Asp Leu Glu
545 550 555 560

Met Leu Ala Pro Tyr Ile Pro Met Asp Asp Asp Phe Gln Leu Arg Ser
565 570 575

Phe Asp Gln Leu Ser Pro Leu Glu Ser Ser Ser Ala Ser Pro Glu Ser
580 585 590

Ala Ser Pro Gln Ser Thr Val Thr Val Phe Gln Gln Thr Gln Ile Gln
595 600 605

Glu Pro Thr Ala Asn Ala Thr Thr Thr Ala Thr Thr Asp Glu Leu
610 615 620

Lys Thr Val Thr Lys Asp Arg Met Glu Asp Ile Lys Ile Leu Ile Ala
625 630 635 640

Ser Pro Ser Pro Thr His Ile His Lys Glu Thr Thr Ser Ala Thr Ser
645 650 655

Ser Pro Tyr Arg Asp Thr Gln Ser Arg Thr Ala Ser Pro Asn Arg Ala
660 665 670

Gly Lys Gly Val Ile Glu Gln Thr Glu Lys Ser His Pro Arg Ser Pro
675 680 685

Asn Val Leu Ser Val Ala Leu Ser Gln Arg Thr Thr Val Pro Glu Glu
690 695 700

Glu Leu Asn Pro Lys Ile Leu Ala Leu Gln Asn Ala Gln Arg Lys Arg
705 710 715 720

Lys Met Glu His Asp GLy Ser Leu Phe Gln Ala Val Gly Ile Gly Thr
725 730 735

Leu Leu Gln Gln Pro Asp Asp His Ala Ala Thr Thr Ser Leu Ser Trp
740 745 750

Lys Arg Val Lys Gly Cys Lys Ser Ser Glu Gln Asn Gly Met Glu Gln
755 760 765

Lys Thr Ile Ile Leu Ile Pro Ser Asp Leu Ala Cys Arg Leu Leu Gly
770 775 780

Gln Ser Met Asp Glu Ser Gly Leu Pro Gln Leu Thr Ser Tyr Asp Cys
785 790 795 800

Glu Val Asn Ala Pro Ile Gln Gly Ser Arg Asn Leu Leu Gln Gly Glu
805 810 815

Glu Leu Leu Arg Ala Leu Asp Gln Val Asn
820 825

<210> 24
<211> 8
<212> DNA
<213> Homo sapiens

<400> 24
bacgtssk

8